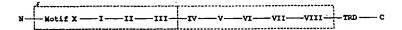
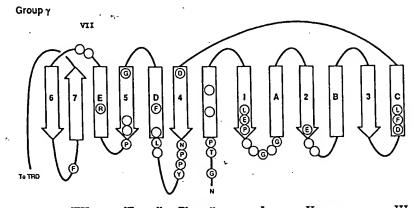
Figure 9 NEW







			VIII	VI	V I	V	x	I		II	1.	11
	Protein		Motif X				Motif I			Motif II		Motif III
			0 0			=	1⇒ Œ	<b>A</b>		==2⇒		=3> CCD
	AccI (N6)	30	Korrie fprayaka	kWI	55	5 1	EPAfolevi:	STAI	77	nikaFeVD	93	eYfdDgenV
	BanIII	16	PahyrytdigdIza	krL	.49	g	DescrideeL	lsL	69	fnnide		keaD rLn
	BsuBI	26	QUITES IS IFMA	cLF	52	2 1	DAGAGICSL	tsAF	79	dlhl	98	alfkbxleI
	CviBIII	26	District rekt	gFt	5	3 11	Escoteel	sec	75	SIKCVELD	100	LVnebruLW
	Eco57I	14	gyyngqnuadyyt	kWV	3	9 2	Ezscudevi.	IAPI	65	cfelFotz	90	tegorivw
	HincII	10	POLITE thinky i	gEM	3	4 📆	Epssoneva	LdsL	55	nltsym	71	VInsSkits
	PaeR7I *	-10	allirseyvdFil	dia.	2:	2 5	Estoced	I PI	83	KreckSaN	100	usqqDriiLa
	PstI	36	GOMSssavseLMa	ngr	6	1 🛱	DAGadvesL	taAF	110	KIRAMEFE	124	II esDrIqa
	TaqI	19	rverppevvdFiv	sia	4	3 📆	EPACAhGo	LTAF	66	REVENTED	85	gilaDrilW
	TthHB8I	17	rverpog vrFm	rg <b>C</b> a	4	1 💆	EPACAdopy	LrAF	64	REVEVED	83	gwadwiiLW
	VspI	116	ever rekeraade	dyL	14	1 F	epeccation.	Liea	181	dev	195	Lekron sa
	EcoRI	50	PrvsnFFkYFavni	dnL	7	9 n	<b>EGF</b> ssseaa	knGF	104	KlvfdDIS	123	sesi <b>D</b> L <b>L</b> kk
,	COMtase	41	nvgdakgqIMdaV	[re¥	6	2 V	<b>LELG</b> ayc <b>G</b> ys	avrM	85	Rlltmemn	117	gaSqDLIpq
	HhaI (C5)	298	GNSVvinVlqyIa	yn <b>l</b> g	1	4 Y	IDLFaGlGgF	rlAL	35	cvysnEWD	56	kpeGDItqv

Protein	Motif IV	Motif V Motif V	'I Motif VII
	<b>⊏</b> 4⇒		
AccI (N6)	117 Down CNPPY fR fhdydn	154 Wittle IKs -hqusqngrcavi	
BanIII	132 Volgannervetovlga	166 prinariva-EtlqLxpcclligVit	
BsuBI	137 ThamlNPPYkKiksnsK	168 Wasasvalty-dlySdcgervii	
CviBIII	113 DETYONPRYVVIPSGYK	141 Mirve LyKcitehikedGilari	EstIg 178 EsklEitldiEsfeE
Eco57I	110 pgalowPreiRyqfleR	149 Manyorulssy-allaqcorrowy	gsels 185 ksylghvcskivk
HinclI	85 postijo NPP v kwknlse	123 DYNYISTIKST-loukvecelist	
PaeR7I	114 TOLVNONPPYVRpelipa	149 DivipoleRsita-USaconLgri	Adrym 185 Erslyaerfhikvy
PstI	146 KwaniNPPTI KiaakgR	177 TrsalValar-kquxscgervar	
TaqI	99 pliffcNPPigivgeasK	141 MINGAGUEKAY-rlikpcovivi	
TthHB8I	97 policoNPPrgivgeasK	139 NEXGALLEKSY-rlikeCotty	
VspI	211 DviFtNPPMgRklpkkd	265 ligda Fniasyes RAN lang	validF 310 Enkgcpddqhatic
EcoRI	133 sDiVVtNPPFslfreyld	175 MLIkenkiwlgvhlgRGvsgFI	VPehYe 208 aRidsngnriIspnn
COMtase	135   1DmVF1Dhwk	147 yLpdtLblekcgllrKGtVlLa	DNViVp 183 VRgsssfecthYssYL
HhaI (C5)	72 hDiLcagfPCQAfsisgk	99 tLffdI-aRiV-rekKPkVVFM	ENVknF 136 VKntMnelDYsFhakV

Protein	Motif VIII	MW	Target	Swissprot	
	:6>	*		Accession Number	
AccI (N6)	209 een ddal	🦸 540 aa	<b>GIMKAC</b>	P25201	
BanIII	220 dtk	580 aa	ATCGAT	P22772	
BsuBI	223 rdkankdde	501 aa	disdas	P33563	
CviBIII	194 dkhdacdtn	377 aa	nca	P10835	
Eco57I	202 keiWedtl	540 aa	GIGAAG	P25240	
HincII	177 eskynhgvs	502 aa	CHYRAC	P17744	
PaeR7I	203 dtpaghsdv	531 aa	dicarc	P05103	
PstI	232 rksarkasd	507 aa	dicare	P00474	
TaqI	. 192 lge <mark>ve</mark> pqkk	421 aa	TCGN	P14385	
TthHB8I	190 lgevepgrk	428 aa	TCGA	P25749	
VspI	333 sqr <b>y</b> jeknp	408 aa	TAATELA	Q03055	
EcoRI	228 nldVFirhk	325 aa	GAATTC	P00472	
COMtase		221 aa	catechol	P22734	
HhaI (C5)	161 QkReRiymi	327 aa	GCGC	P05102	

•	NXXXXKXXLXELVXKYEXXRSTXLXSTYNETXLRSD
BpmIRM AculRM BsgIRM ThaRM	10 20 30 40
	FLDPLFELLGWDXXNXXGTNXXXREVIXEEXLEX EEXX
BpmIRM AculRM BsgIRM ThaRM	50 60 70 80  FI DPLLKSLGWDVDNTKGKTHI LRDVI QEEYI EI KDEETK 70 YLDPFFELLGWDI KNKAGKPTNEREVVLEEALKASASEHS 76 FLDPFFELFGWEMRPERI TNPADLEVI I EESLET EKST 75 FI EPLFKSLGWNFSNRGKTNDS VSAEETI SK 72
	KXPDYTFRI NGTRKFFVEAKKP- SENI XKXXKXAFQARRY
BpmIRM AcuIRM BsgIRM ThaRM	90 110 120  KNPDYTLRI NGTRKLFVEVKKP- SFNI LKSAKAAFQTRRY 109  KKPDYTFRLFSERKFFLEAKKP- SVHI ESDNETAKQVRRY 115  KYI DYVFKI NRTTQFLVEAKKP- AESLSK- KDHI FQAKSY 113  KRVDYGFRI NGI PKFFLEAKPLREENI QNNSKYVTQAI DY 111
	GFTAXLXI SVLTNFEXLVI YDXSXKPDXXD- XXXKARXKX
BpmIRM AculRM BsgIRM ThaRM	130 140 150 160 GWSANLGI SVLTNFEHLVI YDCRYTPDKSD- NEHI ARYKV 148 GFTAKLKI SVLSNFEYLVI YDTSVKVDGDD- TFNKARI KK 154 AFTTEI PFVI LTNFKEFRFYDVSTEPLHNQPDTDKVEEYC 153 AWMKSCSWAI LTNFETVAVYNADWKESNYG S- NLL 145
	FXYXEYEXXFDEIXDLLSREAVXSGXLDKXXXK
BpmIRM AcuIRM BsgIRM ThaRM	170 180 190 200  FSYEEYEEAFDEI KDI I SYESANSGALDEMFD 181  YHYTEYETHFDEI CDLLGRESVYSGNFDKEWLS 188  FDYKEYVQNFDKLWELFSREAVANRSLAKFYAKRRNI VDS 193  FI LHPNDFLTDERFKYLSKKAFENGELDKI ASK 179
	YXNKXXXXXDXXFLQQIXXWREXLAEXIXKN
BpmIRM AcuIRM BsgIRM ThaRM	210 220 230 240VNTRVGETFDEYFLQQI ENWREKLAKTAI KN 211I ENKI NHFSVDTLFLKQI NTWRLLLGEEI YKY 219 PDLI FKLNYQI DKGASLLDI SFLKNLKI WRKSLAENI FNN 233YGKKQLKNPI DKQLLQDMI HFREVLSKDI VKN 210
	NXXLXENEVNEI VQRI LDRLI FLRVCEDRNLEXYETLK
BpmIRM AculRM BsgIRM ThaRM	250 260 270 280  NT ELGEEDVNFI VQRLLNRI I FLRVCEDRTI EKYETI K 249  QP TI QENELNDI VQSYLNRI I FLRVCEDRNLETYQTLL 257  N SLNVNVI NEVVQRI LDRLI FI RI I EDRNI ESKEFLK 270  NQDKHLTQDEVDESVQRI LDRLI FI RNAEDRGLEENQLQS 250



moriday, potobor		•
•	XI XXXXE	XXELXDLFKXXDRKFNSGLFDFXDHT
BpmIRM AcuIRM BsgIRM ThaRM	NFASSND EI VEMHEQDNSI	300 310 320YEELKDLFQKSDRKFNSGLFDFIDDT 279FSALIDKFKQADRCYNSGLFDQLLTE 290 SVKNELDKLCIELNKKFNGLVFHDHT 308 HLMKEISRIYKDFDDKYNSKLFAHH 286
	LXXEXXI DNEVL	IVIIXXLYYPKSPYDFSVIXSDILG
BpmIRM AculRM BsgIRM ThaRM	330 LLLEVEI DSNVL QI I EDI SS VF FVNEALI DNEI L	340 350 360 I EI FSDLYFPQSP YDFSVVDPTI LS 316 WVI I KQLYYPESP YSFSVFSSDI LG 325 I VI I DNLYYPKSP YNFRLI KPEI LG 345 QEVI EGLNHSKDDSYRYDFSVI ESDVLG 326
	NI YEXFLGEKI X	I EXGKTXLXXKXXNXXX GVVYTPSYI
BpmIRM AculRM BsgIRM ThaRM	370 QI YERFLGQEII NI YEI FLSEKLV RI FEQFLGEKI E	380 I ESGGTFHI TESPEVAASNGVVPTPKI I 356 I NQSRVELVKKPENLDR DI VTTPTFI 363 BOXA II DGKI TLGLKDI NKKSG- GVYYTPSYI 384 KLEESKTHRKEQ GI YYTPSYI 357
		XX-GKTXEELXQLKI ADI ACGSGSFLIS
BpmIRM AculRM BsgIRM ThaRM	VEKI VENTUSKK	420 TE- GKKFNELCNLKI ADI CCGSGTFLIS 395 Box B CCY- GKTDI EI LQLKFADI ACGSGAFLLE 402 KLHNDI TI ENLEQI KI ADI ACGSGSFLIS 424 Moff I K- THTPEEI KKVRI LDPACGSGSFLIR 396
	SYKXLXDKXXXX	(YXXXXDDSQLVXXXXGXLXLT
BpmIRM AcuIRM BsgIRM ThaRM	450 SYDFLVEKVMEH LFQLLNDTLVDY SYKYLI DKFQYI	460 470 480  KIIEENI DDSDLVYETEEGLILT 429  YYLSSDTSQLIPTGI GTYKLS 434  YSKCSEADVQTLI SNNLVFI DNGKLMLT 464  NSDFAQLTLDSEEF 421
		FGVDXDPXAVEVAKLSLLLKLLEGE X
BpmIRM AculRM BsgIRM ThaRM	490 LKAKRNI LENNI YEI KRKVLLSCI MEHKKGI LQQNI YSKKVEI LRNNI	FGI DKDLNAVEAAKFGLLLKLLEGEDVQ 474 FGVDI DSQAI QVAKLSLYI TMLEEG Y 502(Maif)
		PILPDLXDNI KXGNSLXDN PEXL
BpmIRM AcuIRM BsgIRM ThaRM	530 SVNNFI HEHEDI SI ANI R I REGTL R I	540 550 560  KILPDLTSIIKCGNSLVDNKFFEFMPESL 509 Box PVLPDLLDNILFGNSLLEPEKV 502 PILPDLNDNIKHGNSIIDNEIL 530 (Maif

•	Santa - Mai - Mai Fal - Santoria and Market Mai - Market Mai - Mai
BpmIRM AculRM BsgIRM ThaRM	EDDXI XXDXNX FEWE FPDI MXNGGFDVI I GNPPYV  570
BpmIRM AculRM BsgIRM ThaRM	RI QNMKXXXPXEXXXYXKK YXVAAKKNFDI YFLFI EK  610 620 630 640  RI QNMKKYSPEEI EYYQSKDSEYTVAKKETVDKYFLFI ER 586 FOXF KSEDMKNI TPLELPLYKKN YVSAYKQFDKYFLFLER 566, RI QI FEELYGKDVVNYLKK KYVSAEKFNFDI YVVFI EK 608 (MANF) RI QNLNDE ETGWFNKT FKSAYKNYDI YLLFVEK 543
BpmIRM AcuIRM BsgIRM ThaRM	ALXLLNEXGILGYIVPSKFFXTXYGKKLRELITEKKXLYK  650  ALILLNPTGLLGYIIPHKFFITKGGKELRKFIAEKHQISK GLALLKEEGILGYIVPSKFTKVGAGKKLRELLTDKGYLDS 606  ALSLLNDQGILGYIVMNKFFTTQYGEKLRELITSQKLLYE 648 SFDLCKENGIIGFIIPSKFINAYYGLGLRNLISETKSLYK 583  BOX G / Mo FF II)  BOX G / Mo FF II)
BpmIRM AcuIRM BsgIRM ThaRM	II DFGXNQI FXDAATYTCI LI LXKTKXDXFKYXXVXNLXT  690 700 720  II NFGVTQVFPGRATYTAI LI I QANKMAQFKYKKVSNI SA 666 BOX I I VSFGANQI FQDKTTYTCLLI LRKTPHTDFKYAEVRNLI D 646  II DFGI NEI FNNATTYTCI LI LDKTNPDEI I I ERVI DLNT 688 MAN I DFKDVQI FGDAANYTCI LFLKI YKNDVFSYI FPKSTDT 623
BpmIRM AculRM BsgIRM ThaRM	WTXXSXSNXXVXSXXXLXSDPWILSSNEXEEVYXKF 730 740 750 760 ETLDSEENTCVYSSEKYNSDPWIFLSPETEAVFTKF 702 WKVRKADAMEFSSQQLSTLQSDAWILIPSELISVYHQI 684 WKAGESSDRKVVDHTEFTSTPWYLSSNTDEEIYKFF 724 FTIQSVSNVDTFQEYKLPLPKPDHPWILSENKVSELIRKL 663
BpmIRM AculRM BsgIRM ThaRM	XEXXXXLEXIS-IDNIFVGLQTSADXVYIFXPEXETXDTY  770 780 790 800  TEAQFEKLGEITDISVGLQTSADKIYIFIPENETSDTY 740 LAQSQKLEDIVGIDNIFNGIQTSANDVYIFVPTHEDTENY 724 EENMVLLETISDRVFVGVQTDCDPVYILEEVYEEENYL 762 SRKGIPLEIISKNIFQSLTTSADGIYFVQVESETRDTA 701
BpmIRM AculRM BsgIRM ThaRM	YFXKKGXEYKIEKXILKPXLKGXSIXXYXXXXN  810 820 830 840  IFNYKGKRYEIEKSICCPAIYDLSFGSFESIQGN 774  YFIKKGQEYKIEKEITKPYFKTTSGEDNLYTYRTFKPN 762  YCKSEYTTEVHKFEKDHLKPFLKGSLDIKKYTFSNVN 799  KIRNIKNNLEFAVEKTILRKLLKGKDIRRCSVDWKG 737

,	AXVI FPYTXXDXXAXLI PLXTI KXXFPLAYKYLXSXKEXL	
BpmIRM AcuIRM BsgIRM ThaRM	ARVIYPYTQTESSVELIPLDEIREIFPLAYKYLMSLKFVL KWLLFPYTNSENTSDLIPETTYKQYFPETWKYLESCKERL	814 802 839 777
	XX- KRSI XXR XNEWHQYGRXQSL XKFX- QXKI VX	
BpmIRM AcuIRM BsgIRM ThaRM	890 900 910 920 EKRSLQGRNPKWYQYGRSQSLSKFHDKEKLIW SSPKRDIKPRPKTTNEWHRYGRHQSLDNCGLSQKIIV AK-RKSIERELDINPNYNEWYKYIYKKNHTRMD-QLKIVF	846 839 877 810
	XVLAXGXXFAI DXNG FLFSGGGNGGGXXI VLPDQSXY	
BpmIRM AcuIRM BsgIRM ThaRM	930 940 950 960 TVLATKPPYVLDRNN LLFTGGGNG PYYGLI NQSI Y GVLSVGDKYAI DTYG TLI SSGGTAGYCVVALPDDCKY	881 876 917 848
	SYYYLLGI LNSXVLEXXXKXRGSXFRGGYYSXGKKFI ENL	
BpmIRM AcuIRM BsgIRM ThaRM	970 980 990 1000  SLHYFLGI LSHPVI ESMVKARASEFRGSYYSHGKQFI EKI SI YYLQAI LNSKYLEWFSALHGEVFRGGYI ARGTKVLKNL NYLSLLGI LNSEVVSYQI VRRGSKHKGSYYGVDKKRI ENL MYYFVLALLNSNVLEFYLKNI STPFRGGYFSYGKRFI DKL	921 916 957 888
	PI RKI DFDNX- E- NLFDXV\$TXVKELI XI XDKI XXXXNTD	
BpmIRM AcuIRM BsgIRM ThaRM	10'10 10'20 10'30 10'40 PI RKI DFDDQDEVDKYNTVVTTVEKLI I TTDRI KSESNGP PI RKI DFDNLEEANLHDLI ATKQKELI EI YDKI DVNVNNK YVPLI NEDNK NLFSNI SKMVAQI LDAFQKMHQAGTTD PLLI PKD SRFDSVSSLSKEQMNI SKKMRNFPNTD	961 956 994 922
	RRX-XLQRRXDXLXXXLNQLIYELYNLXVEEXTXXXNXLX	
BpmIRM AculRM BsgIRM ThaRM	1050 1060 1070 1080 RRR- MLRRRLDALSNQLI QVI NELYNI SDEEYTTVLNDEM RVLTPLQRMFKREKEVLDQLLSRLYNLGVDDSLI PYI KDL VGKEQLQQRI KMLNARI NELVYRLYNLPVEYKEYI KNALE ERD- LLEREYDKRCQELNQMI YEI YGLNKLEI TLLDDRLC	1000 996 1034 961
	X-A	
BpmIRM AculRM BsgIRM ThaRM	LTAALGEEK YEAH N Q	1009 1000 1035 962